

PEDV In The Pigs Of Montana

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Emergence of Porcine Epidemic Diarrhea in Montana

In 2013, the Montana State Veterinary Diagnostic Laboratory (MSVDL) received fecal samples from a commercial swine facility that was experiencing severe diarrhea in neonatal and growing pigs. The farm reported high morbidity and mortality in piglets. The clinical presentation was consistent with porcine epidemic diarrhea virus (PEDV), which had recently emerged in the United States (Stevenson et al., 2013). The laboratory investigation aimed to confirm infection and characterize the viral strain.

Sample Collection and PCR Detection

Fecal and intestinal samples were collected from affected pigs and tested using reverse-transcription polymerase chain reaction. Viral RNA was extracted, converted into complementary DNA, and amplified with primers targeting PEDV genes. The samples produced positive PCR results, confirming the presence of PEDV. Other enteric pathogens were considered in the differential diagnosis because diarrhea in pigs can be caused by transmissible gastroenteritis virus, rotavirus, bacteria, and parasites.

Spike Gene Analysis and Viral Variation

The spike protein is important for viral entry into host cells and for immune recognition. Sequence analysis of the spike gene can help compare strains and identify mutations (Chen et al., 2014). The Montana samples were sequenced and compared with PEDV sequences available from other locations. Similarity to strains circulating in the United States suggested a common introduction or rapid spread through animal movement, transport vehicles, feed ingredients, equipment, or human activity.

Vaccine Effectiveness and Viral Evolution

Genetic changes in the spike gene may influence antigenicity and vaccine performance. Existing vaccines may not provide complete protection when circulating strains differ from vaccine strains. However, sequence differences alone do not prove that a vaccine will fail. Protection also depends on maternal immunity, vaccination timing, herd exposure, biosecurity, and the ability of sows to transfer

antibodies through colostrum and milk. Continued surveillance is necessary to monitor viral evolution and evaluate control measures.

Phylogenetic Comparison of PEDV Strains

Phylogenetic analysis places related viral sequences into groups based on genetic similarity. The Montana strain clustered with contemporary North American PEDV isolates rather than older European vaccine strains. This supported epidemiological evidence that the outbreak was connected to the recent emergence of PEDV in the United States. Phylogenetic findings can help trace transmission patterns, although they must be interpreted with farm histories and movement data.

Detection of PEDV in Sow Milk

Samples of milk and mammary secretions from infected sows were also examined. PEDV RNA detection in milk does not necessarily mean that infectious virus is transmitted through milk because PCR can identify nonviable genetic material. Nevertheless, the finding raises questions about how piglets are exposed. Contamination of teats, skin, the farrowing environment, and equipment with fecal material may allow oral infection during nursing.

Potential Vertical Transmission and Farm Control

Evidence for true vertical transmission of PEDV from the sow to piglets before or through birth remains limited. The major route of spread is fecal-oral transmission (Jung et al., 2020). Control therefore depends on strict biosecurity, cleaning and disinfection, control of vehicle and personnel movement, separation of infected animals, management of manure, and development of herd immunity. Rapid laboratory diagnosis and genetic monitoring help farms respond to outbreaks and reduce losses.

References

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